

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:02:29 ; Search time 8.04545 Seconds  
(without alignments)  
3060.813 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCKARKOPIKEEFTAEIHT 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3384	100.0	636	1 P73_HUMAN	O15350 homo sapien
2	3304.5	97.7	631	1 P73_CERAE	O9XSK8 cercoptithec
3	851.5	25.2	396	1 P53_ONCW	P25035 oncorhynchu
4	821	24.3	369	1 P53_BABU	O9W678 barbus barb
5	801.5	23.7	373	1 P53_BRARE	P79734 brachydantio
6	790.5	23.4	386	1 P53_FIG	O9TUB2 sus scrofa
7	789.5	23.3	376	1 P53_ICTPU	O93379 ictalurus p
8	778.5	23.0	381	1 P53_CANFA	O29537 canis famill
9	778	23.0	367	1 P53_CHICK	P10360 gallus gall
10	776	22.9	386	1 P53_FELCA	P41685 felis silve
11	760.5	22.5	386	1 P53_BOVIN	O29628 bos taurus
12	755.5	22.3	382	1 P53_SHEEP	P51664 ovis aries
13	752	22.2	351	1 P53_ORYLA	P79820 oryzias lat
14	750.5	22.2	391	1 P53_CAVPO	O9WUR6 cavia porce
15	749	22.1	396	1 P53_MESAU	O00366 mesocricetu
16	745.5	22.0	393	1 P53_CRIGR	O09185 cricetulus
17	741	21.9	363	1 P53_XENLA	P07193 xenopus lae
18	739.5	21.9	393	1 P53_TUPGB	O9TAL1 tapalia glis
19	736.5	21.8	391	1 P53_MARMO	O36006 marmota mon
20	735.5	21.7	391	1 P53_RAT	P10361 rattus norv
21	731.5	21.6	367	1 P53_TETMU	O9W679 tetraodon m
22	725.5	21.4	393	1 P53_MACMU	P56424 macaca mulla
23	724.5	21.4	391	1 P53_RABIT	O95330 corytolagus
24	724.5	21.4	393	1 P53_HUMAN	P04637 homo sapien
25	723.5	21.4	393	1 P53_MACFA	P56423 macaca fasc
26	718.5	21.2	393	1 P53_CERAE	P13481 cercoptithec
27	711.5	21.0	390	1 P53_MOUSE	P02340 mus musculu
28	695	20.5	366	1 P53_PLAFE	O12946 platichthys
29	691.5	20.4	280	1 P53_HORSE	P79892 equus cabal
30	686.5	20.3	314	1 P53_SPERE	O64662 spermophilu
31	686	20.3	342	1 P53_XIPHE	O57538 xiphophorus
32	686	20.3	342	1 P53_XIPMA	O92143 xiphophorus
33	600.5	17.7	207	1 P53_EQUAS	O29480 equus asinu

34	133	3.9	1273	1	WEB1_YEAST	P38968 saccharomyc
35	131.5	3.9	2459	1	MAPB_RAT	P15205 rattus norv
36	129	3.8	306	1	EXTN_DAUCA	P06599 daucus caro
37	127.5	3.8	784	1	SP4_HUMAN	O02446 homo sapien
38	126.5	3.7	1386	1	ZAP3_MOUSE	O9R017 mus musculu
39	126	3.7	817	1	VRP1_YEAST	P37370 saccharomyc
40	126	3.7	1902	1	SMF1_HUMAN	O14497 homo sapien
41	124.5	3.7	3358	1	PGCV_MOUSE	O62059 mus musculu
42	124	3.7	1051	1	ULK1_MOUSE	O70405 mus musculu
43	124	3.7	1972	1	P531_HUMAN	O12888 homo sapien
44	123.5	3.6	1618	1	NES1_HUMAN	P48881 homo sapien
45	123	3.6	1227	1	LAF4_HUMAN	P51826 homo sapien

## ALIGNMENTS

RESULT 1  
P73\_HUMAN  
ID P73\_HUMAN STANDARD; PRT; 636 AA.  
AC O15350; O15351; Q9NTK8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).  
GN TP73 OR P73.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Colon;  
RX MEDLINE=974333090; PubMed=9288759;  
RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;  
RT "Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";  
RL Cell 90:809-819(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=9289209; PubMed=10362363;  
RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.;  
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";  
RL Oncogene 18:3415-3421(1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=98389621; PubMed=9721206;  
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;  
RT "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";  
RL Genomics 51:359-363(1998).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).  
RX MEDLINE=98021697; PubMed=9802988;  
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annicchiarico-Petruzzelli M., Leviero M., Melino G.;  
RT "Two new p73 splice variants, gamma and delta, with different transcriptional activity.";  
RL J. Exp. Med. 188:1763-1768(1998).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).  
RX MEDLINE=993110938; PubMed=10381648;  
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Leviero M., Knight R.A.;  
RT "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new new splicing variants epsilon and zeta.";

2/3/97/7/3/98

Cell Death Differ. 6:389-399 (1999).  
 [6] SEQUENCE FROM N.A. (ISOFORM KAPPA).  
 RA Thomas D.;  
 RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).  
 RA MEDLINE-99318135; PubMed-10391251;  
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharbanda S., Weichselbaum R., Kufe D.;  
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response  
 to DNA damage.";  
 RL Nature 399:814-817(1999).  
 [8]  
 RP ERRATUM.  
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharbanda S., Weichselbaum R., Kufe D.;  
 RL Nature 400:792-792(1999).  
 [9]  
 RP FUNCTION.  
 RA MEDLINE-99217940; PubMed-10203277;  
 RA Kaelin W.G. Jr.;  
 RT "The emerging p53 gene family.";  
 RL J. Natl. Cancer Inst. 91:594-598(1999).  
 [10]  
 RP STRUCTURE BY NMR OF 439-506.  
 RX MEDLINE-99380160; PubMed-1049409;  
 RA Chi S.W., Ayed A., Arrowsmith C.H.;  
 RT "Solution structure of a conserved C-terminal domain of p73 with  
 structural homology to the SAM domain.";  
 RL EMBO J. 18:4438-4445(1999).  
 CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.  
 WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE  
 PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR  
 PROTEIN.  
 CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL  
 TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY  
 AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA  
 INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA  
 INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS: 7 ISOFORMS: ALPHA (SHOWN HERE), BETA, GAMMA,  
 DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE  
 SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS  
 RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE  
 SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME  
 TO THE ALPHA ISOFORM.  
 CC -!- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,  
 SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.  
 CC -!- INDUCTION: NOT INDUCED BY DNA DAMAGE.  
 CC -!- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA  
 BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS  
 TO THE ABL TYROSINE KINASE SH3 DOMAIN.  
 CC -!- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE  
 CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN  
 HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN  
 NEUROBLASTOMA AND OLIGODENDROGLIOMA.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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Db 541 IWRLQDLKQGHYDGAQAQLRSSNAAISIGSGELQQRVMENVHVRHTIIPNR 600  
QY 600 GPGGGPDWADFGFDLPCKARKKOPIKEEFTAEIH 636  
DB 601 GPGGAGDEWADFGFDLPCKARKKOPIKEEFTAEIH 637

RESULT 3  
P53\_ONCMY  
ID P53\_ONCMY STANDARD; PRT; 396 AA.  
AC P25035;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxId=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210066; PubMed=1339362;  
RA de Fromental C.C., Padkel F., Chapuis A., Baney C., May P., Soussi T.;  
RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";  
RL Gene 112:241-245(1992).  
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION (BY SIMILARITY).  
CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; M75145; AAA49605.1; .  
DR PIR; JH0631; JH0631  
DR HSSP; P04637; 1TUP  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR ProDom; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 44  
FT DNAS\_BIND 90 281  
FT FT DOMAIN 325 356  
FT FT DOMAIN 369 392  
FT BASIC (REPRESSION OF DNA-BINDING).  
FT FT DOMAIN 303 318  
FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 395 395  
FT PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 396 AA; 43966 MW; 84222507655A5C CRC64;

Query Match 25.2%; Score 851.5; DB 1; Length 396;  
Best Local Similarity 55.6%; Pred. No. 6.3e-50;  
Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 150

QY 93 VPTHSPAQRS-STFDTMS-PAPVPISNTDYPGPHEFVTQQSSTAATWTYSPLKK 150  
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FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 66 BY SIMILARITY.  
FT DOMAIN 298 OLIGOMERIZATION.  
FT DOMAIN 329 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 342 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 276 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 368 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;  
  
Query Match 24.3%; Score 821; DB 1; Length 369;  
Best Local Similarity 54.0%; Pred. No. 6.3e-48;  
Matches 169; Conservative 49; Mismatches 83; Indels 12; Gaps 7;  
  
QY 83 SPYTPHEAASVTHSPYAPQSPSTEDTMSAPVIPSNTDYPGPHFHEFTFOOSSTAKSATW 142  
DB 35 SFEPNFDNVTQSP--QPS-----TSPTASVPVAIDYGEHGFGLGFPQSGTAKSVTC 88  
  
QY 143 TYPPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVVKRCNHELGRD 202  
DB 89 TVSSDLNLFCLQAKTCPQVMVNVAPPQGSVIRATAIYKKSEHVAEVRRCPPHHERTPD 148  
  
QY 203 FNEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVPYEPQVGTETTTLYNFMNCSSC 262  
DB 149 -GDG-LAPAAHLIRVEGNLSQYVDDPVTGROSVVVPYEPQVGTETTTLYNFMNCSSC 206  
  
QY 263 VGMNRRPILITILEMRDQVLRGRRSFEGRICACPGDRKADDEHYREOQALNESSAKN 322  
DB 207 MGNMRRPILITILEMRDQVLRGRRSFEGRICACPGDRKADDEHYREOQALNESSAKN 265  
  
QY 323 GAASHRAF-KOSPAPVAPALGAGVKKRRHG--DETYIYLVQVGRNFEILMKLESLELME 379  
DB 266 PSANKRSTKSTSPVPEGSKKALSGSSDEIYTLQVRGRERYEMLKINDSLSD 325  
  
QY 380 LVPQLVDSYRQO 392  
DB 326 VYPPSEMDRYRQK 338  
  
RESULT 5  
P53\_BRARE  
ID P53\_BRARE STANDARD; PRT; 373 AA.  
AC P79734;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (tumor suppressor p53).  
GN TP53.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97344388; PubMed=9200835;  
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,  
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;  
RT "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and  
RT expression during embryogenesis";  
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).  
CC -1- GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION (BY SIMILARITY).  
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----  
DR EMBL; U60804; ABA0617.1;  
DR HSP; P04637; ITUP.  
DR ZFIN; ZDB-GENE-990415-270; tp53.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 70 260 BY SIMILARITY.  
FT DOMAIN 301 332 OLIGOMERIZATION.  
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FF CRC64;  
  
Query Match 23.7%; Score 801.5; DB 1; Length 373;  
Best Local Similarity 51.0%; Pred. No. 1.3e-46;  
Matches 158; Conservative 50; Mismatches 91; Indels 11; Gaps 5;  
  
QY 85 YTPHEASVTHSPYAPQSPSTEDTMSAPVIPSNTDYPGPHFHEFTFOOSSTAKSATW 144  
DB 41 FDPNFFENLEEQ--QPS-----TLPSTVPTSDYDGHGFLRFPQSGTAKSVTCY 94  
  
QY 145 SPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHVTDVVKRCNHELGRDN 204  
DB 95 SPDLNLFCLQAKTCPQVMVNVAPPQGSVIRATAIYKKSEHVAEVRRCPPHHE--RTPD 152  
  
QY 205 EQSAPASHLIRVEGNLSQYVDDPVTGROSVVVPYEPQVGTETTTLYNFMNCSSCVG 264  
DB 153 GDLNAPAGHLIRVEGNLSQYVDDPVTGROSVVVPYEPQVGTETTTLYNFMNCSSCVG 212  
  
QY 265 GMRNRRPILITILEMRDQVLRGRRSFEGRICACPGDRKADDEHYREOQALNESSAKNGA 324  
DB 213 GMRNRRPILITILEMRDQVLRGRRSFEGRICACPGDRKADDEHYREOQALNESSAKNGA 271  
  
QY 325 ASKRAFQSPVAPVAPALGAGVKKRR--HGDETYIYLVQVGRNFEILMKLESLELME 382  
DB 272 GTRSLVRESSATLRPEGSKKAGSSSDEIYTLQVRGRERYEMLKINDSLSDVVP 331  
  
QY 383 QPLVDSYRQO 392  
DB 332 ASDAEKRYRQK 341  
  
RESULT 6  
P53\_PIG  
ID P53\_PIG STANDARD; PRT; 386 AA.  
AC Q9TUB2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cellular tumor antigen p53 (tumor suppressor p53).  
GN TP53 OR P53.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;  
RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

[illegible]

QY 204 NEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPYEPQVGTERTTILYNFMCNCSV 263  
 DB 161 SDG-PAPGHLIRVEGNSRAVYQDNGTQARSVVVPPYEPQVGSQTTLVYNYMCSNM 219  
 QY 264 GMMNRRLPILITLMDRGVLRSPGEGRICACPGDRKADHDHYREQOALNESSAKNG 323  
 DB 220 GMMNRRLPILITLMDRGVLRSPGEGRICACPGDRKADHDHYREQOALNESSAKNG 323  
 QY 324 AASKRAFQSPAPVAPALGAGVKKRRHGDDETYLQVRGNEFELMLKLESLELMELVQ 383  
 DB 277 TLTKRSMK-DPPSHE-ASKKSNSSDDEITYLQVRGKERYEFLKINDGLELSQVWP 334  
 QY 384 PLVDSYRQ 392  
 DB 335 ADQEKYRK 343

RESULT 8  
 P53\_CANFA STANDARD; PRT; 361 AA.  
 AC Q29537; Q9TV78;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cellular tumor antigen p53 (tumor suppressor p53).  
 GN TP53 OR P53.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=98178696; PubMed=9519881;  
 RA "Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein."  
 RT Oncogene 16:1077-1084(1998).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Spleen;  
 RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T., Watarai T., Hasagawa A., Tsujimoto H.;  
 RT "Aberrations of p53 tumor suppressor gene in various spontaneous tumors in the dog."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 25-300 FROM N.A.  
 RC STRAIN=BEAGLE;  
 RX MEDLINE=95323915; PubMed=7600529;  
 RA Kragel S.A., Pazzi K.A., Madewell B.R.;  
 RT "Sequence analysis of canine p53 in the region of exons 3-8."  
 RL Cancer Lett. 92:181-186(1995).  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.  
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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CC EMBL; AF060514; AAC16909.1; -  
 CC EMBL; AB020761; BAA78379.1; -  
 CC EMBL; S77819; ABA42022.1; -  
 CC HSSP; P04637; IOLG  
 CC InterPro: IPR002117; P53.  
 CC Pfam: PF00870; P53; 1.  
 CC PRINTS; PR00386; P53SUPPRESSOR.  
 CC PRODOM; PD002681; P53; 1.  
 CC PROSITE; PS00348; P53; 1.  
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 89 280 BY SIMILARITY.  
 FT DOMAIN 313 344 OLIGOMERIZATION.  
 FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 2 4 EES -> QSP (IN REF. 2).  
 FT CONFLICT 378 378 L -> P (IN REF. 2).  
 FT CONFLICT 381 AA; 42486 MW; 761A/18FDC93DA59 CRC64;  
 SQ SEQUENCE 381 AA; 42486 MW; 761A/18FDC93DA59 CRC64;  
 Query Match 23.0%; Score 778.5; DB 1; Length 381;  
 Best Local Similarity 44.1%; Pred. No. 4.6e-45;  
 Matches 165; Conservative 57; Mismatches 93; Indels 59; Gaps 8;

QY 14 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVFLHGMTTSYMAQFNLLSSTDW 73  
 DB 18 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVFLHGMTTSYMAQFNLLSSTDW 73  
 QY 74 QMSRAASAPYTPHRAASVTPHSPYAPQSPSTEDTSPAPVIPSNTDYPGPHFEVTFQ 133  
 DB 59 DAPRMPATASATAPGAPSPWPLSSS-----VPSKTYPTCYGRLGFLH 102  
 QY 134 SSTAKSATWYSPLKLYCOIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHVTDVVR 193  
 DB 103 SGTAKSATWYSPLKLYCOIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHVTDVVR 162  
 QY 194 CNHELGRDFNEGQAPASHLIRVEGNLSQYVDDPVTGRQSVVVPYEPQVGTERTTIL 253  
 DB 163 CPHHERCSDSDG-LAPQHLIRVEGNLRAKYLDDRTFRHSVVVPPYEPQVGSQDTH 221  
 QY 254 YNFMNCSGCGMNRRLPILITLMDRGVLRSPGEGRICACPGDRKADHDHYREQ 313  
 DB 222 YNFMNCSGCGMNRRLPILITLMDRGVLRSPGEGRICACPGDRKADHDHYREQ 278  
 QY 314 ALNESSAKNG-----AASKRAFQSPAPVAPALGAGVKKRRHGDDETYLQVRGNEF 365  
 DB 279 -----KKGECPEPPPGSTKRALPPSTSSPP-----QKKPLDGEYFTLOIRGRY 326  
 QY 366 EILMLKESLELME 379  
 DB 327 EMFRNLNEALEKD 340

RESULT 9  
 P53\_CHICK STANDARD; PRT; 367 AA.  
 ID P53\_CHICK  
 AC P10360;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.







**us-09-125-005-6.rsp**

SEQUENCE FROM N.A.  
SPECIES-B, indicus; STRAIN-BORAN; TISSUE-Blood;  
Bishop R.R.P., Gohright E.E.I.;  
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CIRCUMSTANCES OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
EXPRESSION.  
-1- SUBUNIT: BINDS AS AN HOMOTETRAMER (BY SIMILARITY).  
-1- SUBCELLULAR LOCATION: Nuclear.  
-1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
IN MANY TYPES OF CANCER.  
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; X81704; CAA57348.1; -  
EMBL; D49825; BAA08629.1; -  
EMBL; U74486; AAB51214.1; -  
HSSP; F04637; 1YCR  
InterPro; IPR002117; P53.  
Pfam; PF008070; P53; 1.  
PRINTS; PR00386; P53SUPPRESSR.  
ProDom; PD002681; P53; 1.  
PROSITE; PS00348; P53; 1.  
Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNAS\_BIND 94 285 BY SIMILARITY.  
FT FT 318 349 OLIGOMERIZATION.  
FT FT 361 380 BASIC (REPRESSION OF DNA-BINDING).  
FT FT 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT FT 385 385 PHOSPHORYLATION (BY SIMILARITY).  
FT MOD\_RES 380 380 R -> T (IN REF. 2).  
FT CONFLICT 380 380  
FT SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;  
Query Match 22.5%; Score 760.5; DB 1; Length 386;  
Best Local Similarity 44.2%; Pred. No. 7.4e-44;  
Matches 169; Conservative 63; Mismatches 105; Indels 45; Gaps 11  
QY 60 SYVAQENLLSYTDQMSSRAASASPT-----PEHAASVPTHS-PTAQPSTFTDM 109  
Db 24 NLLPENLLSS-----EUSAPVDLLPTDVATWLDCEPNEAQMPEPSAAPPPAT--- 76  
QY 110 SPAPV-----IPSTNDYDPGHFEVTFQOSTAKSATWTYSPLKLYCQIAKTCPI 161  
Db 77 -PAPATSWPLSSFPVSQKTYPGNYGFLGFLQSGTAKVTCTYSPSLKFLCQIAKTCPV 135  
QY 162 QIKVSTPPPGTAIRAMPYTKAEHVDVVKPCPNHELGRDFNEGOSAPASHLRVSGNN 221  
Db 136 QLWYDPPPPGTVRMAIYKLEHTEVVRRCPCPHERSSDSIG-LAPPOHLLRVSGNL 194  
QY 222 LSOYVDDPVTGROSVVVPYEPQVGTFTILYNFMCNCSVCGGMNRRPILIIITLMDR 281  
Db 195 RAEVLDRNTFRISVVVVPYESPIDESECTIHYNFMCSNCGMGNRRPILITILEDSC 254  
QY 282 GOVLGRRSFEGRTACGRRDRKADEHYREQ-QALNESSAKNGAASKAFKQSPYAPAL 340  
Db 255 GNLIGRNSFEVRCACPGRRRTTEENLRKKGQSCPEPPPR---STKRALPTNTSSSQ- 310

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QY      341 GAGVKKRRHGDETYTQLQVRGRENFEILMKLKESLELMELYPQLVDYSRQQOOLLQRS   400
Db      ::::KPLDGEYFTLQIRGKRVEFMRELDALELKDAL-----DGREPGEGRAHSS   360
QY      401 HLQP-----PSYGPVLSPNNVHG   419
Db      ::::KPKRPSPSCHKKPMLKREG   382

```

RESULT 12  
P53 SHEEP

ID	PS3_SHEEP	STANDARD;	PRT;	382 AA.
DR	PS1664;			
DR	01-OCT-1996 (Rel. 34, Created)			
DR	01-OCT-1996 (Rel. 34, Last sequence update)			
DR	16-OCT-2001 (Rel. 40, Last annotation update)			
EN	Cellular tumor antigen p53 (Tumor suppressor p53). TP53.			
EN	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;			
OC	Bovidae; Caprinae; Ovis.			
NCBI	NCBI_TextID:9940;			
EN	[1]			

P SEQUENCE FROM N. A.  
C TISSUE-BLOOD;  
X MEDLINE-95352828; Pubmed=7626788;  
X Dequiedt F., Kettmann R., Burny A., Willens L.;  
T "Nucleotide sequence of the ovine p53 tumor-suppressor cdna and its  
T genomic organization.";  
T DNA Seq. 5:255-259(1995).

**-1- FUNCTION:** ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE. BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS- ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND P53 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.

- 1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
- 1- SUBCELLULAR LOCATION: Nuclear.
- 1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
- 1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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-----

EMBL; X81705; CAA57349.1; -	
HSSP; P04637; LAIE.	
InterPro; IPR002117; P53.	
Pfam; PF00870; P53; 1.	
PRINTS; PR00386; P53SUPPRESSR.	
ProDom; PD002881; P53; 1.	
PROSITE; PS00348; P53; 1.	
Anti-oncogene; DNA-binding; Transcription regulation; Activator;	
Nuclear protein; DNA-binding; Phosphorylation; Apoptosis.	
DOMAIN	1 44
DNA_BIND	90 281
DOMAIN	314 345
DOMAIN	357 376
DOMAIN	300 312
MOD_RES	381 381
SEQUENCE	382 AA; 42809 MW; 48024076C79C3B2D CRC64;

```

Query Match      22.3%; Score 755.5; DB 1; Length 382;
Best Local Similarity 44.8%; Pred. No. 1.6e-43;
Matches 168; Conservative 62; Mismatches 110; Indels 35; Gaps 10;

QY 60 SYMAQNFLLSSTMDDOMSSRAASAPYT-----PEHAASVPTHSHPAQPSSSTDYTM 109
Db 24 NLLPENNLSS---ELSAVDLDLLPYSDVVTWLDCEPNEAQP--EPPAQAALAPATS 78

QY 110 SP-APVIPSNTDYPGPHHFEVTFQOSTAKSATWYSPLLKLYCQIAKTCPIQIRKSTP 168
Db 79 WPLSFFSPSQKTYPGNYGFRGLFGLHSTAKSVCTTSPSLKLFQCLAKTCPVOLWVDS 138

QY 169 PPGCTATRAMPVYKKAHEVTDVVKRCPNHGLRDNFNEGOSAPASHLIRVEGNLSQYVDD 228
Db 139 PPGCTRVRAAIYKKEHMTVEVRRSPHHSSDYS DG-LAPQHLIRVEGNLRABEYFDD 197

QY 229 PVTGROSVVVYPYPPOVGTFTILYNMCNSCVGGMNRRPILIIITLEM RDGOVLGR 288
Db 198 RNTFRHSVVVYSPESIESECTIHYFNMCNSCGMGNRRPILITILED SRGNLLGS 257

QY 289 SFEGRICACPGDRDKADEHYREQ-OALNESSAKINGAASKRAFKOSPPAVPALGAGVKRR 347
Db 258 SFEVRVACPGDRDRRTTEENFRKKGQSCPEPP---GSKRALPSTSSSP-----OKK 309

QY 348 RHGEDTYVLYQVRGRENPEILMKLESLELMBVLPQPLVDYSYRQOQQLQRP SHLOP--- 404
Db 310 KPLDGEYFTLQIRGRKREMPFELNEALEMD-----AQAGREPGESRAHSHLKKKG 363

QY 405 PSYGPVLSPMKNVHG 419
Db 364 PPSCHKKPKMLKREG 378

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RESULT 13
P53_ORYLA
ID P53_ORYLA
AC AC
DT DT
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53

OS Oryzias latipes (Medaka fish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.  
OX NCBI\_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=97305153; PubMed=9161419;  
RA Krause M.K., Rhodes L.D., van Beneden R.J.;  
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka  
RT (Oryzias latipes) and evaluation of mutational hotspots in MNNG-  
RT exposed fish.";  
RL Gene 189:101-106(1997).  
r2

-I- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

-I- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Nuclear.

-I- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR	EMBL; U57306; AAC60146.1; -	
DR	HSSP; P04637; LYCS.	
DR	InterPro; IPR002117; P53.	
DR	Pfam; PF00870; P53; 1.	
DR	PRINTS; PR00386; P53SUPPRESSR.	
DR	ProDom; PD002681; P53; 1.	
DR	PROSITE; PS00348; P53; 1.	
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;	
KW	Nuclear protein; Phosphorylation; Apoptosis.	
FT	DOMAIN	1 47
FT	DNA_BIND	86 272
FT	DOMAIN	301 330
FT	DOMAIN	333 349
FT	DOMAIN	282 294
FT	MOD_RES	350 350
FT	SEQUENCE	351 AA; 39666 MW; BC61533633568BEA1 CRC64:
SQ	TRANSCRIPTION ACTIVATION (ACIDIC). BY SIMILARITY. OLIGOMERIZATION. BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).	

Db 288 RKKGLCPPTPGN---IKRALPTSSSPQ-----PKKKPLDAEYFTLKIRGRKNFEIL 339

QY 369 MKLAKSELMELVQPLVDYSYRQOQLLQRPSSLQPPS 406

Db 340 REINEALEFK-----DAQTEKRGESRPHSSYPKS 369

RESULT 15

PS3\_MESAU STANDARD; PRT; 396. AA.

AC Q00366; P97276;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus

OX NCBI\_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SYRIAN; TISSUE=Kidney;

RX MEDLINE=92210007; PubMed=1555773;

RA Legros Y., McIntyre P., Soussi T.;

RT "The cDNA, cloning and immunological characterization of hamster p53.";

RL Gene 112:247-250(1992).

RN [2]

RP SEQUENCE FROM N.A.

RA Hou E.W., Wiseman R.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE. BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS- ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.

CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC -----

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CC -----

CC EMBL; M75144; AAA37085.1; -

DR EMBL; U07182; AAB41344.1; -

DR PIR; JH0633; JH0633.

DR HSP; P04637; IYCO.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR ProDom; PD002681; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;

KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA\_BIND 105 295 BY SIMILARITY.

FT DOMAIN 328 359 OLIGOMERIZATION.

FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD\_RES 395 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 188 G -> S (IN REF. 2).

SQ SEQUENCE 396 AA; 43631 MW; 906EF02568099BE3 CRC64;

Query Match 22.1%; Score 749; DB 1; Length 396;

Best Local Similarity 43.8%; Pred. NO. 4.5e-43;

Mismatches 165; Conservative 58; Mismatches 104; Indels 50; Gaps 10;

QY 14 TFEHLWSSLEPDSYFDLPPQSSRGNGNEVVGTDSSMDVHFLEGMTTSYMAQFNLLSSTMD 73

Db 18 TFSDLMKLLPPNNVLTLPSS-----DSIEELFLENVA-----GWLEDPGE 59

QY 74 QMSRAASASPTPEHAASVP---THSPYAQPSSTFDNTPAPV---TPSNTDYPGPHEF 127

Db 60 ALOGSAASAPAP--AAEDPVAETAPVASAPAT-----PWPLSSVSPSYKTYGDIYGF 112

QY 128 EVTFQOOSTAKSATWTYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHV 187

Db 113 RLGLHSGTAKSVCTYSPLNKLFCQAKTCVQLWVSTPPPGTVRAMAIYKKLQYM 172

QY 188 TDVYKRCPNHELGRDFNEGOS--APASHLIRVEGNLSQYVDDPVTGRQSVVYPPQVG 246

Db 173 TEVVRCPHHERS---SEGDLAPPQHLIRVEGNMHAETLDDKQTFRHSVVVYPEPEVG 229

QY 247 TEFTILYNFMCNSSCVGGMNRRLIITILEMRDGOVLGRSFEGRICACPGDRKDE 306

Db 230 SDCITIHYNMCNSSCMGMNRRLIITILEDPSGNLLGRNSFEVRICACPGDRRTTE 289

QY 307 DHYREQ----QALNESSAKNGAASKRAFKOSPPAVPALGAGVKKRRHGDDETYLQVGR 362

Db 290 KNFQKKGPCPELPKSAKRALPTNTSSSPQ-----KRLTDCGYFTLKIRGQ 338

QY 363 ENFEILMKLKSLELME 379

Db 339 ERFKMFQELNEALELKD 355

Search completed: November 7, 2002, 10:09:04

Job time : 12.0455 secs